

Thu Aug 1 12:08:43 2002

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 1, 2002, 09:29:47 ; Search time 2881.61 seconds
(without alignments)
130.718 Million cell updates/sec

Title: US-10-014-743-2

Perfect score: 18

Sequence: 1 TGTAAACGACGCCAGT 18

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:

1: gb_ba:

2: gb_htg:

3: gb_in:

4: gb_om:

5: gb_ov:

6: gb_pat:

7: gb_ph:

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12: gb_sv:

13: gb_un:

14: gb_vi:

15: em_ba:

16: em_fun:

17: em_hum:

18: em_in:

19: em_mu:

20: em_om:

21: em_or:

22: em_ov:

23: em_pat:

24: em_ph:

25: em_pl:

26: em_ro:

27: em_sts:

28: em_un:

29: em_vi:

30: em_htg_hum:

31: em_htg_inv:

32: em_htg_other:

33: em_htg_inv:

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	ID	Description
------------	-------	-------	-------	--------	----	-------------

1	18	100.0	18	6	A49774	A49774 Sequence 5
2	18	100.0	18	6	AR007529	AR007529 Sequence
3	18	100.0	18	6	AR012189	AR012189 Sequence
4	18	100.0	18	6	AR016075	AR016075 Sequence
5	18	100.0	18	6	AR022604	AR022604 Sequence
6	18	100.0	18	6	AR023877	AR023877 Sequence
7	18	100.0	18	6	AR024485	AR024485 Sequence
8	18	100.0	18	6	AR030639	AR030639 Sequence
9	18	100.0	18	6	AR030808	AR030808 Sequence
10	18	100.0	18	6	AR036904	AR036904 Sequence
11	18	100.0	18	6	AR038851	AR038851 Sequence
12	18	100.0	18	6	AR044721	AR044721 Sequence
13	18	100.0	18	6	AR052368	AR052368 Sequence
14	18	100.0	18	6	AR055166	AR055166 Sequence
15	18	100.0	18	6	AR059043	AR059043 Sequence
16	18	100.0	18	6	AR065059	AR065059 Sequence
17	18	100.0	18	6	AR068722	AR068722 Sequence
18	18	100.0	18	6	AR079674	AR079674 Sequence
19	18	100.0	18	6	AR080255	AR080255 Sequence
20	18	100.0	18	6	AR085312	AR085312 Sequence
21	18	100.0	18	6	AR086107	AR086107 Sequence
22	18	100.0	18	6	AR089515	AR089515 Sequence
23	18	100.0	18	6	AR092061	AR092061 Sequence
24	18	100.0	18	6	AR112196	AR112196 Sequence
25	18	100.0	18	6	AR112299	AR112299 Sequence
26	18	100.0	18	6	AR116140	AR116140 Sequence
27	18	100.0	18	6	AR122269	AR122269 Sequence
28	18	100.0	18	6	AR128087	AR128087 Sequence
29	18	100.0	18	6	AR131243	AR131243 Sequence
30	18	100.0	18	6	AR141143	AR141143 Sequence
31	18	100.0	18	6	AR149238	AR149238 Sequence
32	18	100.0	18	6	AR150714	AR150714 Sequence
33	18	100.0	18	6	AR151387	AR151387 Sequence
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37	18	100.0	18	6	AR161623	AR161623 Sequence
38	18	100.0	18	6	AR166046	AR166046 Sequence
39	18	100.0	18	6	AR166075	AR166075 Sequence
40	18	100.0	18	6	AR166716	AR166716 Sequence
41	18	100.0	18	6	AR166982	AR166982 Sequence
42	18	100.0	18	6	AR168734	AR168734 Sequence
43	18	100.0	18	6	AR176654	AR176654 Sequence
44	18	100.0	18	6	AR178163	AR178163 Sequence
45	18	100.0	18	6	AX027591	AX027591 Sequence

ALIGNMENTS

RESULT	1	A49774	Sequence 5 from Patent WO9609395.	18 bp	DNA	linear	PAT 07-MAR-1997
LOCUS	A49774	Sequence 5 from Patent WO9609395.					
DEFINITION	A49774	Sequence 5 from Patent WO9609395.					
ACCESSION	A49774	Sequence 5 from Patent WO9609395.					
VERSION	A49774.1	GI:2303068					
KEYWORDS		unidentified.					
SOURCE		unidentified.					
ORGANISM		unclassified.					
REFERENCE		1 (bases 1 to 18)					
AUTHORS		Meyer, T.F., Pohlner, J., Beck, S.C., Jose, J., Woeik, U., Lorenzen, D.R.					
TITLE		and Oetzelberger, K.B.					
JOURNAL		DRUG FOR THE PREVENTION AND TREATMENT OF AUTO-IMMUNE AND VIRAL					
COMMENT		DISEASES, AND DIAGNOSTIC AGENTS FOR DETECTING SAID DISEASES					
FEATURES		Patent: WO 9609395-A 5 28-MAR-1996;					
		MAX PLANCK GESELLSCHAFT (DE)					
		Other publication AU 3651595 960409.					
		Location/Qualifiers					
		1..18					
		/organism="unidentified"					
		/db_xref="taxon:32644"					
BASE COUNT		6 a	4 c	5 g	3 t		

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Best Local Similarity 100.0%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAAACGACGGCCAGT 18
|||||
DB 1 TGTAAACGACGGCCAGT 18

RESULT 2

LOCUS AR007529 AR007529 18 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 2 from patent US 5750868.
ACCESSION AR007529
VERSION AR007529.1 GI:3967013
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 18)
AUTHORS Cigan,A.M. and Albertsen,M.C.
TITLE Reversible nuclear genetic system for male sterility in transgenic plants

JOURNAL Patent: US 5750868-A 2 12-MAY-1998;
FEATURES Location/Qualifiers
source 1..18
BASE COUNT 6 a 4 c 5 g 3 t
ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAAACGACGGCCAGT 18
|||||
DB 1 TGTAAACGACGGCCAGT 18

RESULT 3

LOCUS AR012189 AR012189 18 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 2 from patent US 5763243.
ACCESSION AR012189
VERSION AR012189.1 GI:3970179
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 18)
AUTHORS Cigan,A.M. and Albertsen,M.C.
TITLE Reversible nuclear genetic system for male sterility in transgenic plants

JOURNAL Patent: US 5763243-A 2 09-JUN-1998;
FEATURES Location/Qualifiers
source 1..18
BASE COUNT 6 a 4 c 5 g 3 t
ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAAACGACGGCCAGT 18
|||||
DB 1 TGTAAACGACGGCCAGT 18

RESULT 4

LOCUS AR016075 AR016075 18 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 3 from patent US 5776680.
ACCESSION AR016075
VERSION AR016075.1 GI:3972352
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 18)
AUTHORS Leibowitz,M.J. and Liu,Y.

TITLE Diagnostic probes for pneumocystis carini
JOURNAL Patent: US 5776680-A 3 07-JUL-1998;
FEATURES Location/Qualifiers
source 1..18
BASE COUNT 6 a 4 c 5 g 3 t
ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAAACGACGGCCAGT 18
|||||
DB 1 TGTAAACGACGGCCAGT 18

RESULT 5

LOCUS AR022604 AR022604 18 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 2 from patent US 5792853.
ACCESSION AR022604
VERSION AR022604.1 GI:3976666
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 18)
AUTHORS Cigan,A.M. and Albertsen,M.C.

TITLE Reversible nuclear genetic system for male sterility in transgenic plants
JOURNAL Patent: US 5792853-A 2 11-AUG-1998;
FEATURES Location/Qualifiers
source 1..18
BASE COUNT 6 a 4 c 5 g 3 t
ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAAACGACGGCCAGT 18
|||||
DB 1 TGTAAACGACGGCCAGT 18

RESULT 6

LOCUS AR023877 AR023877 18 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 2 from patent US 5795753.
ACCESSION AR023877
VERSION AR023877.1 GI:3977171
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 18)

AUTHORS Cigan, A.M. and Albertsen, M.C.
TITLE Reversible nuclear genetic system for male sterility in transgenic plants
JOURNAL Patent: US 5795753-A 2 18-AUG-1998;
FEATURES Location/Qualifiers
source 1..18
BASE COUNT 6 a 4 c 5 g 3 t
ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAAACGACGGCCAGT 18
Db 1 TGTAAACGACGGCCAGT 18

RESULT 7
LOCUS AR024485 18 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 26 from patent US 5795976.
ACCESSION AR024485
VERSION AR024485.1 GI:3977779
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Oefner, P., Josef, and Underhill, P. Anton.
TITLE Detection of nucleic acid heteroduplex molecules by denaturing high-performance liquid chromatography and methods for comparative sequencing
JOURNAL Patent: US 5795976-A 26 18-AUG-1998;
FEATURES Location/Qualifiers
source 1..18
BASE COUNT 6 a 4 c 5 g 3 t
ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAAACGACGGCCAGT 18
Db 1 TGTAAACGACGGCCAGT 18

RESULT 8
LOCUS AR030639 18 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 1 from patent US 5861287.
ACCESSION AR030639
VERSION AR030639.1 GI:5943853
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Metzker, M.L. and Gibbs, R.A.
TITLE Alternative dye-labeled primers for automated DNA sequencing
JOURNAL Patent: US 5861287-A 1 19-JAN-1999;
FEATURES Location/Qualifiers
source 1..18
BASE COUNT 6 a 4 c 5 g 3 t
ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAAACGACGGCCAGT 18
Db 1 TGTAAACGACGGCCAGT 18

RESULT 9
LOCUS AR030808 18 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 11 from patent US 5861378.
ACCESSION AR030808
VERSION AR030808.1 GI:5944022
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Iwanaga, S., Kawabata, S.-I., and Saito, T.
TITLE Horseshoe crab hemocyte polypeptides, and preparation and DNA encoding thereof
JOURNAL Patent: US 5861378-A 11 19-JAN-1999;
FEATURES Location/Qualifiers
source 1..18
BASE COUNT 6 a 4 c 5 g 3 t
ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAAACGACGGCCAGT 18
Db 1 TGTAAACGACGGCCAGT 18

RESULT 10
LOCUS AR036904 18 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 2 from patent US 5800996.
ACCESSION AR036904
VERSION AR036904.1 GI:5954760
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Lee, L.G., Spurgeon, S.L. and Rosenblum, B.
TITLE Energy transfer dyes with enhanced fluorescence
JOURNAL Patent: US 5800996-A 2 01-SEP-1998;
FEATURES Location/Qualifiers
source 1..18
BASE COUNT 6 a 4 c 5 g 3 t
ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAAACGACGGCCAGT 18
Db 1 TGTAAACGACGGCCAGT 18

RESULT 11
LOCUS AR038851 18 bp DNA linear PAT 29-SEP-1999

DEFINITION Sequence 3 from patent US 5807702.
 ACCESSION AR038851
 VERSION AR038851.1 GI:5958214
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 18)

AUTHORS Mukerji, P., Thurmond, J. Marie., Hansson, L., Baxter, J. Harris. and Hards, R. George.

TITLE Method for expressing phosphorylated recombinant human

JOURNAL .beta.-casein in a bacterial system

Patent: US 5807702-A 3 15-SEP-1998;

Location/Qualifiers

source 1..18

BASE COUNT 6 a 4 c 5 g 3 t

ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 18;

Best Local Similarity 100.0%; Pred. No. 30;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAAACGACGCCAGT 18

Db 1 TGTAAACGACGCCAGT 18

RESULT 12

AR044721

LOCUS

DEFINITION Sequence 40 from patent US 5817515.

ACCESSION AR044721

VERSION AR044721.1 GI:5966186

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 18)

AUTHORS Gallatin, W. Michael. and Van der Vieren, M.

TITLE Human B2 integrin alpha subunit antibodies

JOURNAL Patent: US 5817515-A 40 06-OCT-1998;

Location/Qualifiers

source 1..18

BASE COUNT 6 a 4 c 5 g 3 t

ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 18;

Best Local Similarity 100.0%; Pred. No. 30;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAAACGACGCCAGT 18

Db 1 TGTAAACGACGCCAGT 18

RESULT 13

AR052368

LOCUS

DEFINITION Sequence 40 from patent US 5831029.

ACCESSION AR052368

VERSION AR052368.1 GI:5975732

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 18)

AUTHORS Gallatin, W. Michael. and Van der Vieren, M.

TITLE Human .beta.2 integrin .alpha. subunit

JOURNAL Patent: US 5831029-A 40 03-NOV-1998;

FEATURES
 source Location/Qualifiers
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BASE COUNT 6 a 4 c 5 g 3 t

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 30;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAAACGACGCCAGT 18

Db 1 TGTAAACGACGCCAGT 18

RESULT 14

AR055166

LOCUS

DEFINITION Sequence 40 from patent US 5837478.

ACCESSION AR055166

VERSION AR055166.1 GI:5980743

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 18)

AUTHORS Gallatin, W. Michael. and Van der Vieren, M.

TITLE Method of identifying modulators of binding between and VCAM-1

JOURNAL Patent: US 5837478-A 40 17-NOV-1998;

Location/Qualifiers

source 1..18

BASE COUNT 6 a 4 c 5 g 3 t

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 30;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAAACGACGCCAGT 18

Db 1 TGTAAACGACGCCAGT 18

RESULT 15

AR059043

LOCUS

DEFINITION Sequence 2 from patent US 5837851.

ACCESSION AR059043

VERSION AR059043.1 GI:5984620

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 18)

AUTHORS Cigan, A. M. and Albertsen, M. C.

TITLE DNA promoter 5126 and constructs useful in a reversible nuclear genetic system for male sterility in transgenic plants

JOURNAL Patent: US 5837851-A 2 17-NOV-1998;

Location/Qualifiers

source 1..18

BASE COUNT 6 a 4 c 5 g 3 t

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 30;

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us-10-014-743-2.rge

Thu Aug 1 12:08:43 2002

Db 1 TGTAAACGACGCCAGT 18

Search completed: August 1, 2002, 09:29:50
Job time: 6596 sec

Thu Aug 1 12:08:43 2002

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 1, 2002, 09:37:26 ; Search time 365.16 Seconds
(without alignments)
84,633 Million cell updates/sec

Title: US-10-014-743-2

Perfect score: 18
Sequence: 1 TGTAAACGAGCCAGT 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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24: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	18	100.0	18	AAQ39606	Fluorescence detec
2	18	100.0	18	AAQ39606	Fungus-derived 18S
3	18	100.0	18	AAQ39606	hMLH1 gene exon 16
4	18	100.0	18	AAQ39606	M13 primer. Synth
5	18	100.0	18	AAQ39606	Primer RO-4 for be
6	18	100.0	18	AAQ39606	Primer for amplify
7	18	100.0	18	AAQ39606	Defensin coding se
8	18	100.0	18	AAQ39606	5'-Terminal amine
9	18	100.0	18	AAQ39606	Tagged M13 sequenc

10	18	100.0	18	AAQ39606	5'-Terminal amine
11	18	100.0	18	AAQ39606	Primer M13-21 for
12	18	100.0	18	AAQ39606	Primer used in pre
13	18	100.0	18	AAQ39606	Human recombinant
14	18	100.0	18	AAQ39606	Human recombinant
15	18	100.0	18	AAQ39606	Energy transfer fl
16	18	100.0	18	AAQ39606	Human neuroblastom
17	18	100.0	18	AAQ39606	Human K+ channel g
18	18	100.0	18	AAQ39606	Human AMY gene det
19	18	100.0	18	AAQ39606	Human NB Phox dete
20	18	100.0	18	AAQ39606	Human neuro-D gene
21	18	100.0	18	AAQ39606	FER-3 primer for f
22	18	100.0	18	AAQ39606	Hepatitis C virus
23	18	100.0	18	AAQ39606	Mouse alpha-d PCR
24	18	100.0	18	AAQ39606	Human CS198 DNA pr
25	18	100.0	18	AAQ39606	Nucleotide sequenc
26	18	100.0	18	AAQ39606	L105 EST-specific
27	18	100.0	18	AAQ39606	Primer 21M13, used
28	18	100.0	18	AAQ39606	Mouse beta-integri
29	18	100.0	18	AAQ39606	DNA analysis metho
30	18	100.0	18	AAQ39606	Human PS112 gene p
31	18	100.0	18	AAQ39606	Oligonucleotide us
32	18	100.0	18	AAQ39606	Primer based on F1
33	18	100.0	18	AAQ39606	Mammaglobin univer
34	18	100.0	18	AAQ39606	Forward primer for
35	18	100.0	18	AAQ39606	Human MLH1 gene PC
36	18	100.0	18	AAQ39606	Insecticidal toxin
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39	18	100.0	18	AAQ39606	HCV-1b ISD core re
40	18	100.0	18	AAQ39606	M13-21 primer used
41	18	100.0	18	AAQ39606	Oligonucleotide, p
42	18	100.0	18	AAQ39606	Human pancreatic p
43	18	100.0	18	AAQ39606	Human BS274 protei
44	18	100.0	18	AAQ39606	PCR primer for Hum
45	18	100.0	18	AAQ39606	Human alpha-7 nico

ALIGNMENTS

RESULT 1
AAQ39606
ID AAQ39606 standard; DNA; 18 BP.

AC AAQ39606;

DT 07-OCT-1993 (first entry)

DE Fluorescence detection primer KWL.

DE Polymerase chain reaction; PCR; amplify; primer; fluorescence;
KW detection; label; ss.

OS Synthetic.

PN JP05111399-A.

PD 07-MAY-1993.

PF 22-OCT-1991; 91JP-0274264.

PR 22-OCT-1991; 91JP-0274264.

PA (HITA) HITACHI LTD.

DR WPI; 1993-184819/23.

PT Fluorescence detection for nucleic acid sample - comprises
PT binding labelled oligonucleotide(s) to sample DNA, preparing
PT elongation chain by enzyme reaction, isolating different
PT fragments and detecting fluorescence

PS Disclosure; Page 6; 7pp; Japanese.
 CC The sequences given in AAQ39604-09 are primers which were used in a
 CC detection method to detect nucleic acid molecules. The primers are
 CC fluorescently labelled. They are bound to a target nucleic acid
 CC sample and elongated by PCR. The fluorescence of the amplified
 CC sample is detected. This method can be used for the accurate
 CC detection of nucleic acid sequences.
 XX
 SQ Sequence 18 BP; 6 A; 4 C; 5 G; 3 T; 0 other;
 Query Match 100.0%; Score 18; DB 14; Length 18;
 Best Local Similarity 100.0%; Pred. No. 3.4; Mismatches 0; Indels 0; Gaps 0;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TGTAAACGACGCGCCAGT 18
 DB 1 tgtaaacgacgcccagt 18
 RESULT 2
 AAT02863
 ID AAT02863 standard; DNA; 18 BP.
 XX
 AC AAT02863;
 XX
 DT 14-MAR-1996 (first entry)
 XX
 DE Fungus-derived 18S rRNA encoding DNA sequencing primer.
 XX
 DE Polymerase chain reaction; primer; ribosomal RNA; amplification;
 KW sequencing; Matsutake mushroom; ss.
 KW
 OS Agaricus bisporus.
 XX
 PN JP07177889-A.
 XX
 PD 18-JUL-1995.
 XX
 PF 22-DEC-1993; 93JP-0346106.
 XX
 PR 22-DEC-1993; 93JP-0346106.
 XX
 PA (RIKA) RIKAKAKU KENKYUSHO.
 XX
 DR WPT; 1995-279918/37.
 XX
 PT Oligo:nucleotide primer comprising amplification and sequencing
 PT portions - useful for determination of fungal DNA sequences by PCR
 PT amplification
 PS Claim 2; Page 2; 8pp; Japanese.
 XX
 CC AAT02855-T02860 are amplification primers for DNA coding for
 CC fungus-derived 18S rRNA. These primers may be bound at the 5' end
 CC to the 3' end of a sequencing primer (AAT02861-T02863). The
 CC resulting oligonucleotide primers comprising amplification and
 CC sequencing portions (AAT02864-T02869). These primers are useful for
 CC the determination of the base sequences of fungi.
 XX
 SQ Sequence 18 BP; 6 A; 4 C; 5 G; 3 T; 0 other;
 Query Match 100.0%; Score 18; DB 16; Length 18;
 Best Local Similarity 100.0%; Pred. No. 3.4; Mismatches 0; Indels 0; Gaps 0;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TGTAAACGACGCGCCAGT 18
 DB 1 tgtaaacgacgcccagt 18

RESULT 3
 AAQ09024
 ID AAQ09024 standard; DNA; 18 BP.
 XX
 AC AAQ09024;
 XX
 DT 05-MAR-1996 (first entry)
 XX
 DE hMLH1 gene exon 16 second stage amplification primer N-19269.
 XX
 KW hMLH1; MutL homologue; cancer diagnosis; mismatch repair; tumour;
 KW susceptibility; mutation detection; exon 16; primer N-19269;
 KW second stage amplification; ss.
 XX
 OS Synthetic.
 XX
 PN WO9516793-A1.
 XX
 PD 22-JUN-1995.
 XX
 PF 16-DEC-1994; 94WO-US14746.
 XX
 PR 09-DEC-1994; 94US-0352902.
 PR 17-DEC-1993; 93US-0168877.
 PR 08-MAR-1994; 94US-0209521.
 XX
 PA (DAND) DANA FARBER CANCER INST INC.
 PA (UYOR-) UNIV OREGON HEALTH SCI.
 XX
 PI Baker SM, Bollag RJ, Bronner CE, Kolodner RD, Liskay RM;
 XX WPI; 1995-231583/30.
 DR
 XX
 PT Determn. of a mutation in a mutL homologue or gene prod. in a tissue
 PT - used to diagnose cancer susceptibility, and to identify and
 PT classify a DNA mismatch-repair-defective tumour
 XX
 PS Disclosure; Fig 4B-4; 168pp; English.
 XX
 CC AAQ09024 and AAQ09025 are a primer pair for the 2nd stage amplification
 CC of the hMLH1 (a MutL homologue) gene exon 16. A mutation in an
 CC analogous segment of a hMLH1 or hPMS1 nucleic acid isolated from a
 CC subject, can be detected by comparing it with the above gene
 CC fragment. This method can be used to diagnose cancer susceptibility,
 CC or to identify and classify a DNA mismatch-repair defective tumour.
 XX
 SQ Sequence 18 BP; 6 A; 4 C; 5 G; 3 T; 0 other;
 Query Match 100.0%; Score 18; DB 16; Length 18;
 Best Local Similarity 100.0%; Pred. No. 3.4; Mismatches 0; Indels 0; Gaps 0;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TGTAAACGACGCGCCAGT 18
 DB 1 tgtaaacgacgcccagt 18
 RESULT 4
 AAQ091747
 ID AAQ091747 standard; DNA; 18 BP.
 XX
 AC AAQ091747;
 XX
 DT 28-DEC-1995 (first entry)
 XX
 DE M13 primer.
 XX
 KW Beta-2 integrin alpha-d subunit; antiinflammatory; arteriosclerosis;
 KW inflammatory bowel disease; asthma; polymerase chain reaction;
 KW PCR; primer; ss.
 XX
 OS Synthetic.

PT beta-casein in a bacterial system - encodes an exogenous protein
PT and enzyme which modifies the protein
XX
PS Example 5; Page 28; 58pp; English.
XX
CC To create a single construct designed for secretion of phosphorylated
CC protein to the periplasmic space of a bacterial cell, the beta-casein
CC encoding sequence is put into an expression vector containing a leader
CC sequence that directs protein transport to the periplasm. PCR was
CC performed using the clone resulting from these procedures as the target
CC DNA and primers AAT62669-70. Novel plasmids of the invention comprise a
CC promoter, a sequence encoding an exogenous protein, especially human
CC beta-casein, and a sequence encoding an enzyme which can modify the
CC recombinant beta-casein in a bacterial system. The plasmids are useful
CC to produce a modified recombinant protein in a host cell, partic. human
CC caseins, cell receptor proteins, fatty acylated proteins, mammalian
CC muscle proteins, the gag polyproteins of retroviruses, or mammalian
CC proteins targeted by retroviral src kinases. The method can be used to
CC produce a recombinant human protein useful to inhibit attachment of
CC Haemophilus influenzae to human cells, which can prevent and treat
CC otitis media in children.
XX
SQ Sequence 18 BP; 6 A; 4 C; 5 G; 3 T; 0 other;

Query Match 100.0%; Score 18; DB 17; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTAAACGACGCCAGT 18
Db 1 tgtaaacgacgcccagt 18
|||||

RESULT 6
AAT35004
ID AAT35004 standard; DNA; 18 BP.
XX
AC AAT35004;
XX
DT 28-NOV-1996 (first entry)
XX
DE
XX
KW Plant; sterile; sterility; male; reversible; anther; promoter;
KW pollen formation; ss.
XX
OS Synthetic.
XX
PN WO9617945-A1.
XX
PD 13-JUN-1996.
XX
PF 07-DEC-1995; 95WO-US15229.
XX
PR 07-JUN-1995; 95US-0474556.
PR 08-DEC-1994; 94US-0351899.
XX
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Albertson MC, Cignam AM;
XX
DR WPI; 1996-287189/29.
XX
PT Prodn of reversible male sterility in a plant - by transformation
PT with a construct with regulatory elements and DNA which inhibit
PT pollen formation of function
XX
PS Example 1; Page 33; 94pp; English.
XX
CC A construct comprising a DNA sequence encoding a gene product which
CC inhibits pollen formation or function, an operator controlling its

PN WO9517412-A1.
XX
XX 29-JUN-1995.
XX
PF 21-DEC-1994; 94WO-US14832.
XX
XX 05-AUG-1994; 94US-0286889.
PR 23-DEC-1993; 93US-0173497.
XX
PA (ICOS-) ICOS CORP.
XX
XX Gallatin WM, Van Der Vieren M;
PI WPI; 1995-240603/31.
DR
XX Alpha sub-unit polypeptide of human beta 2 integrin - used to
PT identify potential antiinflammatory agents, for the treatment of
PT graft arteriosclerosis, inflammatory bowel disease, asthma, etc.
XX
PS Example 19; Page 58; 172pp; English.
XX
CC The probe based on human integrin alpha-d clone 19A2 (given in
CC AAQ91712) was used to isolate mouse alpha-d cDNA clones from a thymic
CC oligo dt-primed library in lambda ZAP II. Sequencing of isolated
CC clones was performed using M13 and M13 reverse.1 primers
CC (AAQ91747-48).
XX
SQ Sequence 18 BP; 6 A; 4 C; 5 G; 3 T; 0 other;

Query Match 100.0%; Score 18; DB 16; Length 18;
Best Local Similarity 100.0%; Pred. NO. 3.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAAACGACGCCAGT 18
Db 1 tgtaaacgacgcccagt 18
|||||

RESULT 5
AAT62669
ID AAT62669 standard; DNA; 18 BP.
XX
AC AAT62669;
XX
DT 21-MAY-1997 (first entry)
XX
DE
XX
KW Primer RO-4 for beta-casein cDNA amplification.
KW primer; polymerase chain reaction; PCR; plasmid; modified protein;
KW expression; beta-casein; enzyme; kinase; inhibit attachment;
KW Haemophilus influenzae; prevent; treat; otitis media; children; ss.
XX
OS Synthetic.
XX
PN WO9627018-A1.
XX
PD 06-SEP-1996.
XX
PF 27-FEB-1996; 96WO-US02866.
XX
PR 06-NOV-1995; 95US-0554642.
PR 27-FEB-1995; 95US-0395239.
PR 06-NOV-1995; 95US-0554137.
XX
PA (ABBO) ABBOTT LAB.
XX
PI Baxter JH, Hansson L, Hards RG, Mukerji P, Thurmond JM;
XX
DR WPI; 1996-412784/41.
XX
PT Plasmid to express modified recombinant proteins, esp. human

CC expression functionally linked to a promoter specific to cells
 CC critical to pollen formation can be used in the production of male
 CC sterile plants when inserted into plants and expressed. When these
 CC male sterile plants are then crossed with pollen derived from a male
 CC fertility line, make sterile hybrid plants are produced. These
 CC plants can then be made sterile or fertile depending on whether the
 CC incorporated construct is expressed. The method produces reversible
 CC male sterility in a plant. Two primers (AAT35004, AAT35005) were used
 CC to amplify a partial 5126 promoter cDNA clone which was used to
 CC identify a full length clone from a cDNA library.
 XX
 SQ Sequence 18 BP; 6 A; 4 C; 5 G; 3 T; 0 other;

Query Match 100.0%; Score 18; DB 17; Length 18;
 Best Local Similarity 100.0%; Pred. No. 3.4;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGTAAACGACGCCAGT 18
 |||||
 Db 1 tgtaaacgacgcccagt 18

RESULT 7

AAT27188
 ID AAT27188 standard; DNA; 18 BP.

AC AAT27188;

DT 20-NOV-1996 (first entry)

XX Defensin coding sequence primer #1.

XX Structural analogue; defensin; antibacterial; helmet crab;

KW Intrahemocyte fine granule fraction; gram positive; gram negative;

KW fungi; germicide; preservative; wound healing; ss.

XX Synthetic.

OS JP08092286-A.

PN 09-APR-1996.

XX 01-SEP-1994; 94JP-0232025.

XX 22-JUL-1994; 94JP-0191850.

XX (SEGK) SEIKAGAKU KOGYO CO LTD.

XX WPI; 1996-236096/24.

XX Defensin structural analogue peptide(s) - useful as antimicrobial
 PT agents and germicides

XX Example 2; Page 14; 17pp; Japanese.

CC The sequences given in AAT27186-90 are a probe and primers which were
 CC used in the isolation of the full length defensin coding sequence
 CC defensin and it analogues act as antibacterial polypeptides. Peptide
 CC analogues are based on an antibacterial peptide isolated from the
 CC helmet crab intrahemocyte fine granule fraction. They show anti-
 CC bacterial activity against gram positive and gram negative microbes
 CC and fungi. These polypeptides are useful as antibacterial agents,
 CC germicides or as a preservative effective against various microbes.
 CC They are also thought to have wound healing properties. See also
 CC AAR96130-34.

XX Sequence 18 BP; 6 A; 4 C; 5 G; 3 T; 0 other;

Query Match 100.0%; Score 18; DB 17; Length 18;
 Best Local Similarity 100.0%; Pred. No. 3.4;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGTAAACGACGCCAGT 18
 |||||
 Db 1 tgtaaacgacgcccagt 18

RESULT 8

AAT86529
 ID AAT86529 standard; DNA; 18 BP.

XX AAT86529;

XX 05-JUN-1998 (first entry)

XX 5'-Terminal amine linked oligonucleotide.

XX Non-fluorescent label; ligand pair; detection; tag; potentiometry;
 KW cleavage; primer; ss.

XX Synthetic.

XX Key Location/Qualifiers
 FT modified_base 1

FT /*tag= a
 /note= "5'-hexylamine-thymine"

XX WO9727327-A2.

XX 31-JUL-1997.

XX 23-JAN-1997; 97WO-US01070.

XX 21-MAR-1996; 96US-0015402.

XX 23-JAN-1996; 96US-0010436.

XX (DARW-) DARWIN MOLECULAR CORP.

XX Howbert JJ, Mulligan JT, Tabone JC, Van Ness J;

XX WPI; 1997-393711/36.

XX Detection of ligand pair binding and analysis of gene expression -
 PT using tags which are detectable by non-fluorescent spectrometry or
 PT potentiometry

XX Example 4; Page 99; 147pp; English.

CC This oligonucleotide was used in the preparation of tagged M13 sequence
 CC primers. The invention relates to a method for detecting the binding of
 CC a first member to a second member of a ligand pair. It comprises: (a)
 CC combining a set of first tagged members with a biological sample (which
 CC may contain one or more second members) for a time sufficient to permit
 CC binding of a first member to a second member, where the tag is
 CC correlative with a particular first member and detectable by non-
 CC fluorescent spectrometry or potentiometry; (b) separating bound first
 CC and second members from unbound members; (c) cleaving the tag from the
 CC tagged first member; and (d) detecting the tag by non-fluorescent
 CC spectrometry or potentiometry, and thus detecting the binding of the
 CC first member to the second member. Analysing the pattern of gene
 CC expression from a selected biological sample comprises: (a) exposing
 CC nucleic acids from a biological sample; (b) combining the exposed
 CC nucleic acids with one or more tagged nucleic acid probes for a time
 CC sufficient for the probes to hybridise to the nucleic acids, where the
 CC tag is correlative with a particular nucleic acid probe and detectable
 CC by non-fluorescent spectrometry or potentiometry; (c) separating
 CC hybridised probes from unhybridised probes; (d) cleaving the tag from
 CC the tagged fragment; and (e) detecting the tag by non-fluorescent
 CC spectrometry or potentiometry, and thus determining the pattern of gene
 CC expression of the sample. The methods may be used in a wide variety of
 CC assays, including nucleic acid assays (e.g. for diagnostic purposes),
 CC protein-based assays, gene expression analysis, detection of
 CC microorganisms, detection of specific sequences in nucleic acid, or
 CC detection of mutations.

```
XX SQ Sequence 18 BP; 6 A; 4 C; 5 G; 3 T; 0 other;
SQ Sequence 18 BP; 6 A; 4 C; 5 G; 3 T; 0 other;

Query Match 100.0%; Score 18; DB 18; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAAACGACGCCAGT 18
Db 1 tgtaaacgacgccagt 18

RESULT 10
AAV06703
ID AAV06703 standard; DNA; 18 BP.
XX
AC AAV06703;
XX
DT 22-MAY-1998 (first entry)
XX
DE 5'-Terminal amine linked oligonucleotide DMO 767.
XX
KW DNA sequencing; tag; mass spectrometry; non-fluorescent spectrometry;
KW potentiometry; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1
FT /*tag= a
FT /note= "5'-hexylamine-Thymine"
XX
PN W09727331-A2.
XX
PD 31-JUL-1997.
XX
PF 23-JAN-1997; 97WO-US01304.
XX
PR 23-JAN-1996; 96US-0589260.
XX
PR 23-JAN-1996; 96US-0010462.
XX
PA (DARW-) DARWIN MOLECULAR CORP.
XX
PI Howbert JJ, Mulligan JT, Tabone JC, Van Ness J;
XX
DR WPI; 1997-393715/36.
XX
PT Determination of nucleic acid sequences - using tags which are
PT detectable by non-fluorescent spectrometry or potentiometry
XX
PS Example 5; Page 111; 182pp; English.
XX
CC This sequence represents an oligonucleotide shown in the specification.
CC The invention relates to compounds and a method for determining the
CC sequence of a nucleic acid molecule. The method comprises: (a) generating
CC tagged nucleic acid fragments which are complementary to a selected
CC target nucleic acid, where a tag is correlative with a particular
CC nucleotide and detectable by non-fluorescent spectrometry or
CC potentiometry; (b) separating the tagged fragments by sequential length;
CC (c) cleaving the tags from the tagged fragments; and (d) detecting the
CC tags by non-fluorescent spectrometry or potentiometry, and from this
CC determining the sequence. The methods may be used e.g. for determining
CC the sequences of nucleic acid molecules. They may be used for
CC determination of multiple nucleic acid sequences simultaneously. The
CC methods allow sequencing to be performed with enhanced speed and
CC sensitivity.
XX
SQ Sequence 18 BP; 6 A; 4 C; 5 G; 3 T; 0 other;

Query Match 100.0%; Score 18; DB 18; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAAACGACGCCAGT 18
Db 1 tgtaaacgacgccagt 18

RESULT 9
AAV06702
ID AAV06702 standard; DNA; 18 BP.
XX
AC AAV06702;
XX
DT 21-MAY-1998 (first entry)
XX
DE Tagged M13 sequence primer for detection of nucleic acid molecules.
XX
KW Nucleic acid analysis; tag; linker; M13 sequence primer; PCR;
KW non-fluorescent spectrometry; potentiometry; detection; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1
FT /*tag= a
FT /note= "5'-hexylamine-Thymine"
XX
PN W09727325-A2.
XX
PD 31-JUL-1997.
XX
PF 23-JAN-1997; 97WO-US01046.
XX
PR 04-JUN-1996; 96US-0020487.
XX
PR 23-JAN-1996; 96US-0014536.
XX
PA (DARW-) DARWIN MOLECULAR CORP.
XX
PI Howbert JJ, Mulligan JT, Tabone JC, Van Ness J;
XX
DR WPI; 1997-393709/36.
XX
PT Detection and identification of nucleic acid molecules - using tags
PT which may be detected by non-fluorescent spectrometry or
PT potentiometry
XX
PS Example 4; Page 94; 129pp; English.
XX
CC This sequence represents an M13 sequence primer. The invention relates
CC to a method for determining the identity of a nucleic acid (NA)
CC molecule which comprises: (a) generating tagged NA molecules from one or
CC more selected tagged NA molecules, where a tag is correlative with a
CC particular NA fragment and detectable by non-fluorescent spectrometry or
CC potentiometry; (b) separating the tagged molecules by size; (c) cleaving
CC the tag from the tagged molecule; and (d) detecting the tag by non-
CC fluorescent spectrometry or potentiometry, and thus determining the
CC identity of the NA molecule. Detecting a selected NA molecule comprises:
CC (a) combining a tagged NA probe with target NA molecules for a time
CC sufficient to permit hybridisation of the probe to a complementary
CC selected target NA sequence, where the tagged NA probe is detectable by
CC non-fluorescent spectrometry or potentiometry; (b) altering the size of
CC the hybridised tagged probes, the size of unhybridised probes or target
CC molecules, or the size of the probe:target hybrids; (c) separating the
CC tagged probes by size; (d) cleaving the tag from the tagged probe; and
CC (e) detecting the tag by non-fluorescent spectrometry or potentiometry,
CC and thus detecting the selected NA molecule.
XX
```

Qy 1 TGTAAACGACGCCAGT 18
 |||
 Db 1 tgtaaacgacgcccagt 18

RESULT 11
 AAV12872
 ID AAV12872 standard; DNA; 18 BP.

XX AAV12872;
 XX 14-MAY-1998 (first entry)
 XX
 DE Primer M13-21 for M13 DNA sequence.

XX Energy transfer dye; donor dye; acceptor dye; oligonucleotide labelling;
 KW nucleic acid sequencing; fluorescence intensity; M13; PCR primer; ss.
 XX
 OS Synthetic.

XX Key Location/Qualifiers
 FH modified_base 1
 FT /*tag= a
 FT /note= "modified with aminohexyl linkage, to enable
 FT attachment to energy transfer dye"

XX EP805190-A2.
 XX
 PD 05-NOV-1997.
 XX
 PF 02-MAY-1997; 97EP-0303039.
 XX
 PR 04-OCT-1996; 96US-0726462.
 PR 03-MAY-1996; 96US-0642330.
 XX

PA (PEKE) PERKIN-ELMER CORP.
 XX
 PI Lee LG, Rosenblum B, Spurgeon SL;
 XX
 DR WPI; 1997-529051/49.

PT Fluorescent energy transfer dyes - useful for labelling
 PT dideoxynucleotides, oligonucleotides, etc.

PS Example 5; Page 55; 79pp; English.

XX This sequence represents a primer for identifying the M13 sequence shown
 CC in AAV12872. This sequence is labelled with a dye of the invention. The
 CC dye is an energy transfer dyes of formula D-R21-Z1-CO-R22-R28-A (1),
 CC where: D is a donor dye that absorbs light at a first wavelength and
 CC emits excitation energy in response; A is an acceptor dye that absorbs
 CC the excitation energy from D and fluoresces at a second wavelength in
 CC response; Z1 = NH, S or O; R21 = 1-5C alkylene; R22 = an alkene, diene
 CC or alkene group, an unsaturated 5- or 6-membered ring or a fused ring
 CC structure; R28 = a group which includes a functionality to attach the
 CC linker to the acceptor dye. R28 is especially R29-22-CO, where R29 =
 CC 1-5C alkylene and Z2 = NH, S or O. The dyes are used for labelling
 CC nucleosides, nucleoside mono-, di- and triphosphates, oligonucleotides
 CC and oligonucleotide analogues, especially for labelling oligonucleotide
 CC primers or dideoxynucleotides used for nucleic acid sequencing. The dyes
 CC give greater fluorescence intensities than the acceptor dyes alone.

XX Sequence 18 BP; 6 A; 4 C; 5 G; 3 T; 0 other;

Query Match 100.0%; Score 18; DB 18; Length 18;

Best Local Similarity 100.0%; Pred. No. 3.4;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGTAAACGACGCCAGT 18
 |||
 Db 1 tgtaaacgacgcccagt 18

RESULT 12
 AAV04321
 ID AAV04321 standard; DNA; 18 BP.

XX AAV04321;
 XX 20-APR-1998 (first entry)
 XX

DE Primer used in preparation of osteoprotegerin products.

XX Osteoprotegerin; antibody; diagnosis; affinity purification;
 KW recombinant production; transgenic animal; treatment; prevention;
 KW antisense oligonucleotide; probe; detection; screening;
 KW bone disease; osteoporosis; Paget's disease; hypercalcaemia;
 KW hyperparathyroidism; rheumatoid arthritis; osteomyelitis;
 KW osteolytic metastasis; periodontal bone loss; bone necrosis;
 KW osteopaenia; PCR primer; ss.

OS Synthetic.

XX DE19654610-A1.

XX 26-JUN-1997.

XX 20-DEC-1996; 96DE-1054610.

XX 03-SEP-1996; 96US-0706945.

XX 22-DEC-1995; 95US-0577788.

XX (AMGE-) AMGEN INC.

XX Boyle WJ, Calzone FJ, Lacey DL, Chang MS;

XX WPI; 1997-334271/31.

XX Nucleic acid encoding osteoprotegerin - useful for treatment of
 PT diseases involving excessive bone loss, e.g. osteoporosis

PS Example 1; Page 14; 182pp; German.

XX The present sequence is a primer, which was used in the preparation
 CC of osteoprotegerin (OPG) products. Anti-OPG antibodies can be used
 CC in OPG diagnostic assays, and as affinity purification materials.
 CC The OPG cDNA can be used to express recombinant OPG and to generate
 CC transgenic animals. It can also be used to regulate the level of
 CC OPG in mammals, specifically to increase OPG levels, however the
 CC use of antisense sequences is also contemplated. Fragments of the
 CC cDNA can be used as probes to detect OPG expressing cells and
 CC tissue, and to screen cDNA libraries for related sequences. OPG can
 CC be used to treat or prevent bone diseases, specifically excessive
 CC bone loss, e.g. osteoporosis, Paget's disease, hypercalcaemia,
 CC hyperparathyroidism, rheumatoid arthritis, osteomyelitis,
 CC osteolytic metastases, periodontal bone loss, bone necrosis and
 CC osteopaenia.

XX Sequence 18 BP; 6 A; 4 C; 5 G; 3 T; 0 other;

Query Match 100.0%; Score 18; DB 18; Length 18;

Best Local Similarity 100.0%; Pred. No. 3.4;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGTAAACGACGCCAGT 18
 |||
 Db 1 tgtaaacgacgcccagt 18

RESULT 13
 AAT89488
 ID AAT89488 standard; DNA; 18 BP.
 XX

C AAT89488;
 T 20-JAN-1998 (first entry)
 X Human recombinant phosphorylated beta-casein gene PCR primer.
 X
 X Human beta-casein; hBC; phosphorylation; recombinant;
 X PCR primer; Haemophilus influenzae; adhesion; inhibition;
 W infant formula; ss.
 W
 W Synthetic.
 S Homo sapiens.
 S WO9717449-A1.
 X
 X 15-MAY-1997.
 X
 X 06-NOV-1996; 96WO-US17729.
 D
 D
 D
 X 06-NOV-1995; 95US-0554135.
 X
 X (ABBO) ABBOTT LAB.
 X
 X Baxter JH, Hansson L, Hards RG, Mukerji P, Thurmond JM;
 I
 I WPI; 1997-281038/25.
 X
 X Production of recombinant phosphorylated human beta-casein - using
 X plasmid comprising promoter, sequence encoding beta-casein and
 X sequence for phosphorylating kinase
 X
 X Disclosure; Page 34; 51pp; English.
 X
 X This primer is used in PCR amplification for producing beta-casein in
 X E. coli. The amplified fragment after purification is cloned in the
 X expression vector pET-26b and beta-casein in E. coli is produced after
 X further expression and recombination techniques. Such extra cellular
 X localisation eases the purification process of the phosphorylated human
 X beta-casein (hBC). The phosphorylated hBC has the same bioactivity as
 X native hBC as shown by its ability to inhibit the adhesion of
 X H. influenza to human pharyngeal cells. The recombinant phosphorylated
 X hBC can be used in liquid nutritional products, particularly in an
 X infant formula.
 C Note: This sequence designated as SEQ.ID.No.3 in the sequence listing
 C differs from the sequence described as SEQ.ID. No.3 in Example 5
 C (see AAT66778).
 X
 X Sequence 18 BP; 6 A; 4 C; 5 G; 3 T; 0 other;
 X SQ

Query Match 100.0%; Score 18; DB 18; Length 18;
 Best Local Similarity 100.0%; Pred. No. 3-4;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TGTAAACGACGCCCACT 18
 ||||||||||||||||
 Db 1 tgtaaacgacgcccagt 18

RESULT 14
 AAT89489
 ID AAT89489 standard; DNA; 18 BP.
 XX
 AC AAT89489;
 XX
 DT 20-JAN-1998 (first entry)
 XX
 XX Human recombinant phosphorylated beta-casein gene PCR primer.
 DE
 DE Human beta-casein; hBC; phosphorylation; recombinant;
 XX PCR primer; Haemophilus influenzae; adhesion; inhibition;
 KW otitis media; ss.
 KW
 XX

```

XX
PD 27-MAR-1997.
XX
PF 12-AUG-1996; 96WO-US13134.
XX
PR 20-SEP-1995; 95US-0531132.
XX
PA (REGC ) UNIV CALIFORNIA.
XX
PI Glazer AN, Ju J, Mathies RA;
XX
DR WPI; 1997-202806/18.
XX
PT New compounds comprising an energy donor component and an acceptor
PT component - are useful as labels for identifying different nucleic
PT acid sequences in electrophoresis
XX
PS Example; Page 9; 22pp; English.
XX
CC A novel compound comprises an energy donor component (EDC) and an
CC acceptor component (AC), which absorbs energy transferred by the
CC EDC, linked by a backbone comprising sugar phosphate ester monomer
CC linkages with the 1-hydroxyl group being etherified or replaced by
CC a hydrogen. The present sequence, a typical energy transfer
CC fluorescent dye tagged oligonucleotide, was synthesized with
CC donor-acceptor fluorophore pairs separated by six
CC 1',2'-dideoxyribose phosphates. The compound can be used as a label
CC to identify different nucleic acid sequences in electrophoresis
CC separations, and may be prepared using conventional polynucleotide
CC synthetic techniques. When a family of the compounds share a common
CC EDC and spacers, but vary as to the AC, they can be excited at the
CC same wavelength, but exhibit widely spaced emission wavelengths.
XX
SQ Sequence 18 BP; 6 A; 4 C; 5 G; 3 T; 0 other;

Query Match      100.0%; Score 18; DB 18; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAACGACGCCGCT 18
Db 1 tgtaaacgacgccagt 18

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Search completed: August 1, 2002, 09:37:28
Job time: 6764 sec

Thu Aug 1 12:08:44 2002

us-10-014-743-2.rni

Sequence 28, Appl
Sequence 9, Appl
Sequence 3, Appl
Sequence 2, Appl
Sequence 11, Appl
Sequence 1, Appl
Sequence 9, Appl
Sequence 1, Appl
Sequence 85, Appl
Sequence 70, Appl
Sequence 10, Appl
Sequence 74, Appl
Sequence 1, Appl
Sequence 114, Appl
Sequence 85, Appl
Sequence 20, Appl
Sequence 28, Appl

28 18 100.0 18 2 US-08-951-648-28
29 18 100.0 18 2 US-08-964-725-9
30 18 100.0 18 2 US-08-554-137-3
31 18 100.0 18 2 US-09-046-203-2
32 18 100.0 18 2 US-09-018-170-11
33 18 100.0 18 2 US-08-948-364-1
34 18 100.0 18 2 US-09-060-836-9
35 18 100.0 18 2 US-08-715-461-1
36 18 100.0 18 2 US-08-815-448-1
37 18 100.0 18 2 US-08-890-980-85
38 18 100.0 18 3 US-08-589-939-70
39 18 100.0 18 3 US-08-974-022-10
40 18 100.0 18 3 US-08-890-979-74
41 18 100.0 18 3 US-08-873-470-1
42 18 100.0 18 3 US-09-147-550-114
43 18 100.0 18 3 US-08-032-894-85
44 18 100.0 18 3 US-09-071-710-20
45 18 100.0 18 3 US-09-174-437-28

ALIGNMENTS

RESULT 1
US-08-045-758B-1
; Sequence 1, Application US/08045758B
; Patent No. 5451663
; GENERAL INFORMATION:
; APPLICANT: Kang, Hee Chol
; TITLE OF INVENTION: Long Wavelength Chemically Reactive Dipyrrometheneboron
; TITLE OF INVENTION: Difluoride Dyes and Conjugates.
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Molecular Probes, Inc.
; STREET: 4849 Pitchford Avenue
; CITY: Eugene
; STATE: Oregon
; COUNTRY: USA
; ZIP: 97402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch
; COMPUTER: IBM
; OPERATING SYSTEM: MS-DOS 6.0
; SOFTWARE: WordPerfect 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/045.758B
; FILING DATE: 04/08/93
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/786,767
; FILING DATE: 11/01/91
; ATTORNEY/AGENT INFORMATION:
; NAME: Helfenstein, Allegra J.
; REGISTRATION NUMBER: 34,179
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503)465-8300
; TELEFAX: (503)344-6504
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 bases
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Other nucleic acid
; DESCRIPTION: A 5'-amine-derivatized oligonucleotide prepared by automated
; DESCRIPTION: solid phase synthesis.
; HYPOTHEICAL: no
; ANTI-SENSE: no
; US-08-045-758B-1

Query Match 100.0% Score 18; DB 1: Length 18;

GenCore version 4.5
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OM nucleic - nucleic search, using sw model
Run on: August 1, 2002, 09:30:47; Search time 87.24 Seconds
(without alignments)
50.681 Million cell updates/sec

Title: US-10-014-743-2

Perfect score: 18

Sequence: 1 TGTAAACGACGCCAGT 18

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_NA.*
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	1	US-08-045-758B-1
2	18	100.0	18	1	US-08-286-889-40
3	18	100.0	18	1	US-08-494-216-1
4	18	100.0	18	1	US-08-471-601-2
5	18	100.0	18	1	US-08-474-556-2
6	18	100.0	18	1	US-08-554-642-3
7	18	100.0	18	1	US-08-485-618-40
8	18	100.0	18	1	US-08-351-899-2
9	18	100.0	18	1	US-08-479-382-2
10	18	100.0	18	1	US-08-362-652-40
11	18	100.0	18	1	US-08-505-509-3
12	18	100.0	18	1	US-08-470-354-2
13	18	100.0	18	1	US-08-479-383-2
14	18	100.0	18	1	US-08-512-681-26
15	18	100.0	18	1	US-08-726-462B-2
16	18	100.0	18	1	US-08-554-135-3
17	18	100.0	18	1	US-08-605-672-40
18	18	100.0	18	2	US-08-482-293A-40
19	18	100.0	18	2	US-08-943-363-40
20	18	100.0	18	2	US-08-479-041-2
21	18	100.0	18	2	US-08-491-690A-3
22	18	100.0	18	2	US-08-710-330A-7
23	18	100.0	18	2	US-08-540-228-1
24	18	100.0	18	2	US-08-505-617-11
25	18	100.0	18	2	US-08-642-330-2
26	18	100.0	18	2	US-08-432-871C-32
27	18	100.0	18	2	US-08-751-189-9
					Sequence 1, Appl Sequence 40, Appl Sequence 1, Appl Sequence 2, Appl Sequence 3, Appl Sequence 40, Appl Sequence 2, Appl Sequence 2, Appl Sequence 26, Appl Sequence 2, Appl Sequence 40, Appl Sequence 40, Appl Sequence 40, Appl Sequence 40, Appl Sequence 2, Appl Sequence 2, Appl Sequence 7, Appl Sequence 1, Appl Sequence 11, Appl Sequence 2, Appl Sequence 32, Appl Sequence 9, Appl

Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAAACGACGGCCAGT 18
|||||
Db 1 TGTAAACGACGGCCAGT 18

RESULT 2

US-08-286-889-40
; Sequence 40, Application US/08286889
; Patent No. 5470953
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Mich
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 5470953el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Sear Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286,889
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/173,497
; FILING DATE: 23-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: P38,659
; REFERENCE/DOCKET NUMBER: 27866/32168
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-286-889-40

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAAACGACGGCCAGT 18
|||||
Db 1 TGTAAACGACGGCCAGT 18

RESULT 3

US-08-494-216-1
; Sequence 1, Application US/08494216
; Patent No. 5614386
; GENERAL INFORMATION:
; APPLICANT: METZKER, MICHAEL L.
; APPLICANT: GIBBS, RICHARD A.
; TITLE OF INVENTION: ALTERNATIVE DYE-LABELLED PRIMERS FOR
; AUTOMATED DNA SEQUENCING
; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FULBRIGHT & JAWORSKI L.L.P.
; STREET: 1301 MCKINNEY, SUITE 5100
; CITY: HOUSTON
; STATE: TEXAS
; COUNTRY: USA
; ZIP: 77010
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/494,216
; FILING DATE: 23-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BRASHEARS-MACATEE, SARAH J.
; REGISTRATION NUMBER: 38,087
; REFERENCE/DOCKET NUMBER: D-5776
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-651-5151
; TELEFAX: 713-651-5246
; TELEX: 76-2829
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Oligonucleotide"
; HYPOTHETICAL: YES
; POSITION IN GENOME:
; UNITS: 18 bp
US-08-494-216-1

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAAACGACGGCCAGT 18
|||||
Db 1 TGTAAACGACGGCCAGT 18

RESULT 4

US-08-471-601-2
; Sequence 2, Application US/08471601
; Patent No. 5689049
; GENERAL INFORMATION:
; APPLICANT: CIGAN, Andrew M.
; APPLICANT: ALBERTSEN, Marc C.
; TITLE OF INVENTION: Reversible Nuclear Genetic System For
; Male Sterility In Transgenic Plants
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,601
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/351,899
 FILING DATE: 08-DEC-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: BENT, Stephen A.
 REGISTRATION NUMBER: 29,768
 REFERENCE/DOCKET NUMBER: 33229/341/PIHI
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202)672-5300
 TELEFAX: (202)672-5399
 TELEX: 904136
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 18 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-471-601-2

Query Match 100.0%; Score 18; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 0.38;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGTAAACGACGCCAGT 18
 Db 1 TGTAAACGACGCCAGT 18

RESULT 5
 US-08-474-556-2
 Sequence 2, Application US/08474556
 Patent No. 5689051
 GENERAL INFORMATION:
 APPLICANT: CIGAN, Andrew M.
 APPLICANT: ALBERTSEN, Marc C.
 TITLE OF INVENTION: Reversible Nuclear Genetic System For
 TITLE OF INVENTION: Male Sterility In Transgenic Plants
 NUMBER OF SEQUENCES: 23
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Foley & Lardner
 STREET: 3000 K Street, N.W., Suite 500
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20007-5109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/474,556
 FILING DATE: 07-JUN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/351,899
 FILING DATE: 08-DEC-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: BENT, Stephen A.
 REGISTRATION NUMBER: 29,768
 REFERENCE/DOCKET NUMBER: 33229/329/PIHI
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202)672-5300
 TELEFAX: (202)672-5399
 TELEX: 904136
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 18 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-474-556-2

Query Match 100.0%; Score 18; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 0.38;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGTAAACGACGCCAGT 18
 Db 1 TGTAAACGACGCCAGT 18

RESULT 6
 US-08-554-642-3
 Sequence 3, Application US/08554642
 Patent No. 5710044
 GENERAL INFORMATION:
 APPLICANT: Mukerji, P.
 APPLICANT: Thurmond, J.
 APPLICANT: Hansson, L.
 APPLICANT: Baxter, J.
 APPLICANT: Hards, R.
 TITLE OF INVENTION: A Plasmid For Expressing Modified
 TITLE OF INVENTION: Recombinant Proteins in a Bacterial
 TITLE OF INVENTION: System
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Donald O. Nickey
 ADDRESSEE: ROSS Products Division
 ADDRESSEE: Abbott Laboratories
 STREET: 625 Cleveland Avenue
 CITY: Columbus
 STATE: Ohio
 COUNTRY: United States of America
 ZIP: 43215
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: MS-DOS Version 6.21
 SOFTWARE: WordPerfect Version 6.0a
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/554,642
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/395,239
 FILING DATE: 27-FEB-1995
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (614) 624-7080
 TELEFAX: (614) 624-3074
 TELEX: No. 5710044e
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 18 base pairs
 TYPE: Nucleic acid
 STRANDEDNESS: Single
 TOPOLOGY: Linear
 MOLECULE TYPE: DNA
 US-08-554-642-3

Query Match 100.0%; Score 18; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 0.38;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGTAAACGACGCCAGT 18
 Db 1 TGTAAACGACGCCAGT 18

RESULT 7
 US-08-485-618-40
 Sequence 40, Application US/08485618
 Patent No. 5728533
 GENERAL INFORMATION:
 APPLICANT: Gallatin, W. Michael

APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,618
FILING DATE: 21-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32797
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-485-618-40

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TGTAAACGACGGCCAGT 18
|||||
Db 1 TGTAAACGACGGCCAGT 18

RESULT 8
US-08-351-899-2
Sequence 2, Application US/08351899
Patent No. 5750868
GENERAL INFORMATION:
APPLICANT: CIGAN, Andrew M.
APPLICANT: ALBERTSEN, Marc C.
TITLE OF INVENTION: Reversible Nuclear Genetic System For
Male Sterility In Transgenic Plants
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/351,899
FILING DATE: 08-DEC-1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 33229/208/PIHI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-351-899-2

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TGTAAACGACGGCCAGT 18
|||||
Db 1 TGTAAACGACGGCCAGT 18

RESULT 9
US-08-479-382-2
Sequence 2, Application US/08479382
Patent No. 5763243
GENERAL INFORMATION:
APPLICANT: CIGAN, Andrew M.
APPLICANT: ALBERTSEN, Marc C.
TITLE OF INVENTION: Reversible Nuclear Genetic System For
Male Sterility In Transgenic Plants
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,382
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/351,899
FILING DATE: 08-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 33229/339/PIHI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-479-382-2

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGTAAACGACGGCCAGT 18
|||||
Db 1 TGTAAACGACGGCCAGT 18

RESULT 10
US-08-362-652-40
; Sequence 40, Application US/08362652
; Patent No. 5766850
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Sear Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/362,652
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/173,497
; FILING DATE: 23-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,889
; FILING DATE: 5-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 27866/32391
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-362-652-40

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGTAAACGACGGCCAGT 18
|||||
Db 1 TGTAAACGACGGCCAGT 18

RESULT 11
US-08-505-509-3
; Sequence 3, Application US/08505509
; Patent No. 5776680
; GENERAL INFORMATION:
; APPLICANT: Liebowitz, Michael J.
; APPLICANT: Liu, Yong
; TITLE OF INVENTION: Diagnostic Probes for
; TITLE OF INVENTION: Pneumocystis Carinii
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard R. Muccino
; STREET: P.O. Box 1267
; CITY: Princeton
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08551
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/505,509
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/298,087
; FILING DATE:
; APPLICATION NUMBER: US/07/922,987
; FILING DATE: 30-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Muccino, Richard R.
; REGISTRATION NUMBER: 32,538
; REFERENCE/DOCKET NUMBER: UMD1-009
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 466-3407
; TELEFAX: (609) 466-2760
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; US-08-505-509-3

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGTAAACGACGGCCAGT 18
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Db 1 TGTAAACGACGGCCAGT 18

RESULT 12
US-08-470-354-2
; Sequence 2, Application US/08470354
; Patent No. 5792853
; GENERAL INFORMATION:
; APPLICANT: CIGAN, Andrew M.
; APPLICANT: ALBERTSEN, Marc C.
; TITLE OF INVENTION: Reversible Nuclear Genetic System For
; TITLE OF INVENTION: Male Sterility In Transgenic Plants
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA

ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/470,354
APPLICATION NUMBER: US/08/470,354
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/351,899
FILING DATE: 08-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 33229/337/PIHI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-470-354-2

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGTAAACGACGGCCAGT 18
Db 1 TGTAAACGACGGCCAGT 18

RESULT 13
US-08-479-383-2
Sequence 2, Application US/08479383
Patent No. 5795753
GENERAL INFORMATION:
APPLICANT: CIGAN, Andrew M.
APPLICANT: ALBERTSEN, Marc C.
TITLE OF INVENTION: Reversible Nuclear Genetic System For
TITLE OF INVENTION: Male Sterility In Transgenic Plants
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,383
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/351,899
FILING DATE: 08-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 33229/340/PIHI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399

TELEX: 904136
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-479-383-2

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGTAAACGACGGCCAGT 18
Db 1 TGTAAACGACGGCCAGT 18

RESULT 14
US-08-512-681-26
Sequence 26, Application US/08512681
Patent No. 5795976
GENERAL INFORMATION:
APPLICANT: Gelfner, Peter J.
APPLICANT: Underhill, Peter A.
TITLE OF INVENTION: Detection of DNA Heteroduplex Molecules
TITLE OF INVENTION: by Denaturing High Performance Liquid Chromatography and
TITLE OF INVENTION: Methods for Comparative Sequencing
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/512,681
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Evans, Susan T.
REGISTRATION NUMBER: 38,443
REFERENCE/DOCKET NUMBER: 8600-0155
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: 439-MER FORWARD PRIMER
US-08-512-681-26

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Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 TGTAAACGACGGCCAGT 18

RESULT 15
US-08-726-462B-2

Thu Aug 1 12:08:44 2002

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; Sequence 2, Application US/08726462B
; Patent No. 3800996
; GENERAL INFORMATION:
; APPLICANT: Perkin-Elmer Corporation, Applied Biosystems
; APPLICANT: Division
; TITLE OF INVENTION: ENERGY TRANSFER DYES WITH ENHANCED
; TITLE OF INVENTION: FLUORESCENCE
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David J. Weitz, Wilson Sonsini Goodrich
; ADDRESSEE: & Rosati
; STREET: 650 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1050
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Microsoft Windows 3.1/DOS 5.0
; SOFTWARE: Wordperfect for windows 6.0,
; SOFTWARE: ASCII (DOS) TEXT format
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/726,462B
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/642,330
; FILING DATE: May 3, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/672,196
; FILING DATE: June 27, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: David J. Weitz
; REGISTRATION NUMBER: 38,362
; REFERENCE/DOCKET NUMBER: PELM4304
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 493-9300
; TELEFAX: (415) 493-6811
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-726-462B-2

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Query Match ` 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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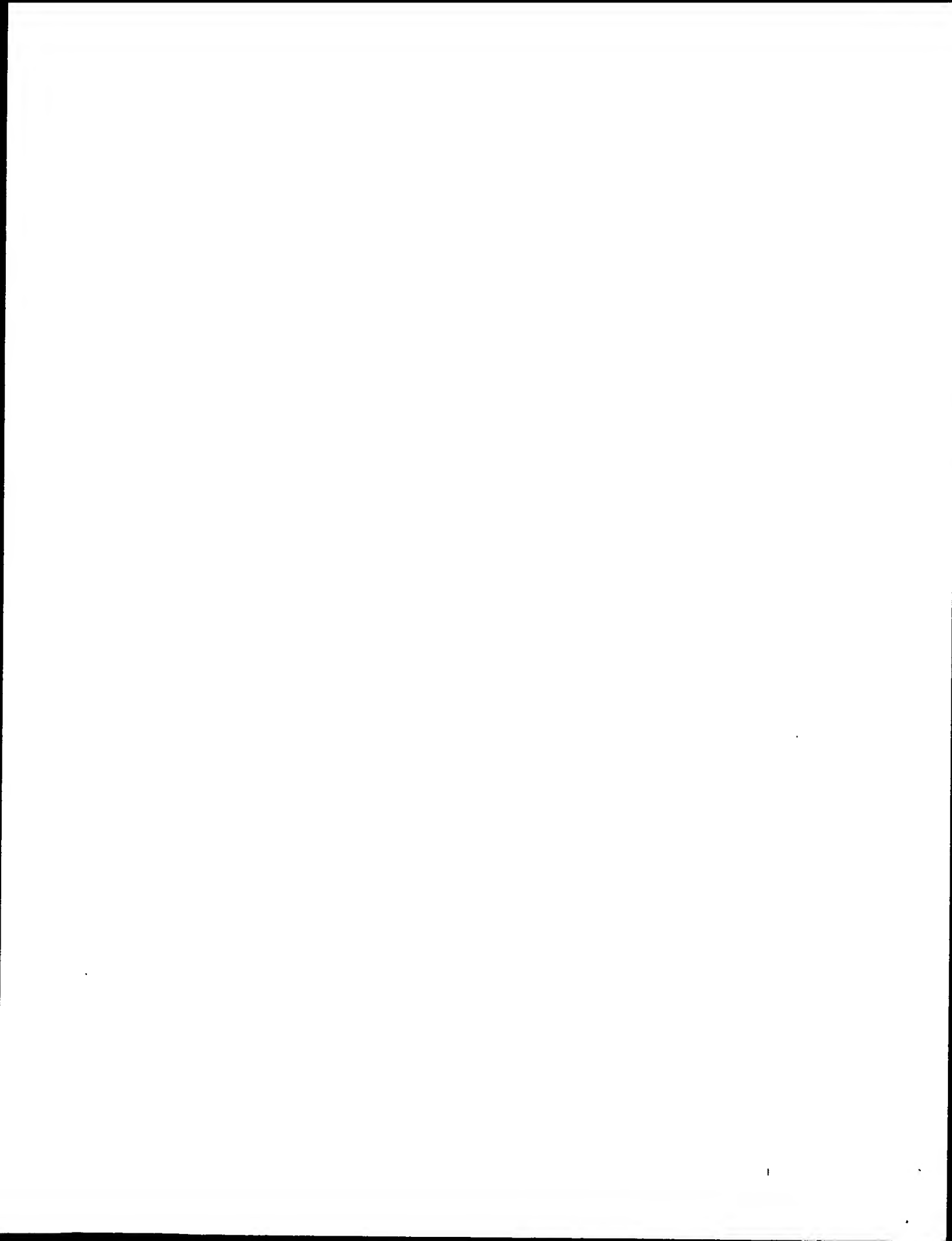
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   |||||
Db 1 TGTAAACGACGGCCAGT 18

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Search completed: August 1, 2002, 09:30:48
Job time: 6609 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 1, 2002, 08:39:40 ; Search time 2971.21 Seconds
(without alignments)
81.766 Million cell updates/sec

Title: US-10-014-743-2

Perfect score: 18

Sequence: 1 TGTAAACGACGCCAGT 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST: *
1: em_estba:*
2: em_esthum:*
3: em_estim:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 4	18	100.0	90	9	AJ239924 AJ239924
C 5	18	100.0	92	10	N28040 EST000177 S
C 6	18	100.0	94	10	BI845735 fs96c02.x
C 7	18	100.0	96	10	R29179 F1-287D 22
C 8	18	100.0	99	10	T10982 hbc297 Huma
C 9	18	100.0	100	9	AA952864 SMTBADA00
C 10	18	100.0	100	9	AA098627 SMTBADA00
C 11	18	100.0	100	9	AW113079 MC7322 mo
C 12	18	100.0	100	9	AW754394 CMO-CT034
C 13	18	100.0	100	9	AW812014 RC6-ST017
C 14	18	100.0	100	9	AW812016 RC6-ST017
C 15	18	100.0	100	10	BF901653 RC4-NT016
C 16	18	100.0	100	12	BH234794 MAA_B03.
C 17	18	100.0	102	9	AA741768 LmLV39p3/

C 18	100.0	103	9	AU180326	AU180326
C 19	100.0	103	9	BE079941	BE079941
C 20	100.0	103	9	AW754393	AW754393
C 21	100.0	108	10	BI716021	BI716021
C 22	100.0	109	10	N28049	N28049
C 23	100.0	110	9	AA728161	AA728161
C 24	100.0	110	9	AA741956	AA741956
C 25	100.0	113	9	AA728380	AA728380
C 26	100.0	113	9	AW749048	AW749048
C 27	100.0	113	9	AW809021	AW809021
C 28	100.0	114	9	AW809013	AW809013
C 29	100.0	115	9	AI940435	AI940435
C 30	100.0	117	9	AW062733	AW062733
C 31	100.0	117	9	BE079985	BE079985
C 32	100.0	118	9	AA804151	AA804151
C 33	100.0	118	9	AW855817	AW855817
C 34	100.0	119	9	AW750572	AW750572
C 35	100.0	120	9	AA864147	AA864147
C 36	100.0	121	10	BI675749	BI675749
C 37	100.0	122	10	N28034	N28034
C 38	100.0	122	12	BH240653	BH240653
C 39	100.0	123	12	BH243317	BH243317
C 40	100.0	125	12	BH471635	BH471635
C 41	100.0	126	9	AA283326	AA283326
C 42	100.0	126	12	BH240234	BH240234
C 43	100.0	127	10	BM129856	BM129856
C 44	100.0	127	10	BM129856	BM129856
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ALIGNMENTS

RESULT 1

AA680645/c
LOCUS
DEFINITION
LmFrAm0099 Leishmania major cDNA clone H02 5', mRNA sequence.
Leishmania major

ACCESSION
AA680645
VERSION
EST.662650

KEYWORDS
SOURCE
ORGANISM
Leishmania major.
Leishmania major
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Leishmania.

REFERENCE
1 (bases 1 to 73)
Norris, A.R., Dvally, S.D., Smith, D.F. and Blackwell, J.M.

AUTHORS
Analysis of Leishmania Major Amastigote Expressed Sequence Tags
Unpublished (1997)
Contact: Blackwell JM
Cambridge Institute for Medical Research
Wellcome Trust/MRC Building, Addenbrooke's Hospital, Hills Road,
Cambridge CB2 2XY, UK
Tel: 01223 336 143
Fax: 01223 331 206
Email: jmb37@cus.cam.ac.uk

PCR Primers
FORWARD: GTAAACGACGCCAGT
BACKWARD: GGAACAGCTATGACCATG
Seq primer: AATTACCTCTACTAAAGG
High quality sequence stop: 72.
Location/Qualifiers
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library"
/cell_type="Amastigote"
/note="Vector: Lambda zap II; Site_1: XhoI; Site_2: NotI"

FEATURES
source

BASE COUNT
ORIGIN
15 a 21 c 18 g 19 t

CONTACT: Chae KS
Faculty of Biological Sciences
Chonbuk National University

100

Eukaryota; Metazoa; Chordata; Cranata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 96)

AUTHORS Choi, S.S., Yun, J.W., Choi, E.K., Cho, Y.G., Sung, Y.C. and Shin, H.S.
TITLE Construction of a gene expression profile of a human fetal liver by single-pass cDNA sequencing
JOURNAL Mamm. Genome 6 (9), 653-657 (1995)
WORD COUNT 62

96081342
Contact: Hee-Sup Shin
Developmental Genetics
Pohang Institute of Science & Technology
San31, Hyojadong Pohang, 790-784 Republic of Korea
Tel: 562-279-2291
Fax: 562-279-2199
Email: shinhs@vision.postech.ac.kr
Seq primer: T3 primer.

FEATURES	Location/Qualifiers
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source	1. .96

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/notes="vector: pBluescriptII SK(-); Site_1: EcoRI; Site_2:
XhoI; The cDNA library made by oligo-dT primed and
directionally cloned between 5' Exor I-XhoI3' sites."
24 a      25 c      17 g      26 t      4 others

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Query Match          100.0%; Score 18; DB 10; Length 96;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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TI0982
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VERSION
GT:391136
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KEYWORDS
human.
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ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 99)
Takeda, J., Yano, H., Eng, S., Zeng, Y. and Bell, G.I.
A molecular inventory of human pancreatic islets: sequence analysis
of 1000 cDNA clones
Hum. Mol. Genet. 2, 1793-1798 (1993)
0430044

3410642/
REDLINE.
COMMENT
Contact: Bell GI or Takeda J
HHMI
Univ. of Chicago
5841 S. Maryland Ave., MC1028, Chicago IL 60637
Tel: 3127029116
Fax: 3127020271
Email: g-bell@uchicago.edu
Seq primer: SK primer.
Location/Qualifiers
1 36
FEATURES
SOURCE

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/db_xref="taxon:9606"
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/note="Vector: Lambda ZAPII; Site_1: Eco RI; Site_2: Xho
I; mRNA was prepared from normal adult human islets. cDNA

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AA098627
VERSION
AA098627.1 GI:1644597
EST
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS

TITLE
JOURNAL
COMMENT

FEATURES
source

AA098627
AA098627.1 GI:1644597
EST
KEYWORDS
SOURCE
ORGANISM
Schistosoma mansoni.
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatidae; Schistosomatidae; Schistosoma.
1 (bases 1 to 100)
Saber M.A., Hamied, H., Elyassaki, W.M., Romeih, M., Ahmed, H., Mohareb
, M., El Dabaa, I. and Mamdouh, S.
Schistosoma mansoni CDNA
Unpublished (1995)
Contact: M.A. Saber, H. Hamied, W.M. El Yassaki, M. Romeih, H.
Ahmed, M. Mohareb, I. El Dabaa, S. Mamdouh
TBRI Biochemistry
Theodor Bilharz Research Institute
Imbaba, P.O.Box 12411, Giza, Egypt
Tel: 202 3128276
Fax: 202 3121167
Email: M-Saber@RCU.EUN.EG
Seq primer: sk.
Location/Qualifiers
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/clone="SMTBADAMS0626SK"
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/note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
XhoI; MRNA was purified from adult couples of S. mansoni.
CDNA was constructed and cloned simultaneously using
vector priming with the pBluescript II SK+ vector. CDNA
was directionally synthesized from the EcoRI site in the
vector to the XhoI site."
21 a 28 c 27 g 24 t

BASE COUNT
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Query Match
Best Local Similarity 100.0%; Score 18; DB 9; Length 100;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TGTAAACGACGGCCAGT 18
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RESULT 11
AW113079/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AW113079
MC7322 mouse liver, vehicle control Mus musculus cDNA clone MC7322
3' similar to U43954 Expression vector pBMRZ, complete cds, mRNA
sequence.
AW113079
AW113079.1 GI:6825792
EST.
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 100)
Thomas, R.S., Rank, D.R., Penn, S.G., Zastrow, G.M., Jovanovich, S. and
Bradfield, C.A.
McArdle Laboratory/Molecular Dynamics Dioxin EST Project
Unpublished (1999)
Contact: Bradfield CA
McArdle Laboratory for Cancer Research
University of Wisconsin
1400 University Ave., Madison, WI 53706, USA
Tel: 608 262 2024
Fax: 608 262 2824
Email: bradfield@oncology.wisc.edu

This clone was sequenced as part of a project to develop a database
on gene expression changes following exposure to various
environmental toxicants. The database can be accessed at
<http://mcarchive.oncology.wisc.edu/bradfield/>. Treatment- dioxane
vehicle (400 ul/kg). Animals sacrificed- 48 hrs post-injection.
Seq primer: dt(23)V (anchored polyT).

FEATURES
source

Location/Qualifiers
1..100
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="MC7322"
/clone_lib="mouse liver, vehicle control"
/sex="male"
/lab_host="JM109"
/note="Organ: liver; Vector: pGEM11zf (Promega); Site_1:
NotI; Site_2: EcoRI; First strand cDNA was primed with a
NotI-polyT primer
15'-AACTGGAGAAATTCGGCCGACGAGGAAATTTTTTTTTTT-3'.
Double-stranded cDNA was ligated with EcoRI adapters
(Pharmacia), digested with NotI, and ligated into the
EcoRI/NotI sites of the pGEM11zf vector. The library was
NOT normalized."
24 a 27 c 21 g 27 t 1 others

BASE COUNT
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 18; DB 9; Length 100;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TGTAAACGACGGCCAGT 18
|||||
Db 49 TGTAAACGACGGCCAGT 32

RESULT 12
AW754394

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

COMMENT

AW754394
CM0-CT0345-021299-114-f11 CT0345 Homo sapiens CDNA, mRNA sequence.
AW754394
AW754394.1 GI:7669326
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 100)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM0&t2=CM0-CT0345-021299-114-f11&t3=1999-12-02&t4=1>)
Seq primer: puc 18 forward
High quality sequence stop: 100.
Location/Qualifiers

FEATURES

source

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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="C70345"
 /dev_stage="Adult"
 /note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
 35 a 24 c 29 g 12 t

BASE COUNT
 ORIGIN

Query Match
 Best Local Similarity 100.0%; Score 18; DB 9; Length 100;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 TGTAAACGACGGCCAGT 18
 Db 33 TGTAAACGACGGCCAGT 50

RESULT 13
 AW812014/C

LOCUS
 DEFINITION RC6-ST0170-291099-012-B02_1 ST0170 Homo sapiens CDNA, mRNA
 ACCESSION AW812014
 VERSION AW812014.1 GI:7905008
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 100)
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

TITLE
 JOURNAL

Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
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 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2-RC6-ST0170-291099-012-B02_1&t3=1999-10-29&t4=1)
 Seq primer: puc 18 forward
 High quality sequence stop: 100.
 Location/Qualifiers
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 /db_xref="taxon:9606"
 /clone_lib="ST0170"
 /dev_stage="Adult"
 /note="Organ: stomach; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of

FEATURES
 source

100.0%; Score 18; DB 9; Length 100;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Query Match
 Best Local Similarity 100.0%; Score 18; DB 9; Length 100;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

tissue mRNA and cDNA amplification were performed under low stringency conditions."
 11 a 29 c 24 g 36 t

Query Match

Best Local Similarity 100.0%; Score 18; DB 9; Length 100;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TGTAAACGACGGCCAGT 18

Db 85 TGTAAACGACGGCCAGT 68

RESULT 14
 AW812016/C

LOCUS
 DEFINITION RC6-ST0170-291099-012-D01_1 ST0170 Homo sapiens CDNA, mRNA
 ACCESSION AW812016
 VERSION AW812016.1 GI:7905010
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 100)
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

TITLE
 JOURNAL

Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br

FEATURES
 source

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2-RC6-ST0170-291099-012-D01_1&t3=1999-10-29&t4=1)
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 High quality sequence stop: 86.
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="ST0170"
 /dev_stage="Adult"
 /note="Organ: stomach; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
 12 a 29 c 23 g 36 t

BASE COUNT
 ORIGIN

100.0%; Score 18; DB 9; Length 100;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Query Match
 Best Local Similarity 100.0%; Score 18; DB 9; Length 100;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAAACGACGCCAGT 18
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Db 68 TGTAAACGACGCCAGT 51

RESULT 15

BF901653
LOCUS RC4-MT0161-091200-011-h01 MT0161 Homo sapiens cDNA, mRNA linear EST 18-JAN-2001
DEFINITION BF901653
ACCESSION BF901653
VERSION BF901653.1 GI:12293112
KEYWORDS EST.
SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 100)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.

TITLE

Shotgun sequencing of the human transcriptome with ORF expressed

JOURNAL

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE

COMMENT

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Ludwig Institute for Cancer Research
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Brazil

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Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC4&t2=RC4-MT0161-091200-011-h01&t3=2000-12-09&t4=1>)

Seq primer: puc 18 forward

High quality sequence stop: 100.

FEATURES

Source

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/db_xref="taxon:9606"
/clone_lib="MT0161"
/dev_stage="Adult"
/note="Organ: marrow; Vector: puc18; Site:1: SmaI; Site:2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
,716 - Ludwig Institute for Cancer Research) profiles
into the puc 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

BASE COUNT 38 a 17 c 33 g 12 t
ORIGIN

Query Match

100.0%; Score 18; DB 10; Length 100;

Best Local Similarity 100.0%; Pred. No. 24;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAAACGACGCCAGT 18

|||||

Db 67 TGTAAACGACGCCAGT 84

Search completed: August 1, 2002, 08:39:47

Job time: 6478 sec

